

Package: marssTMB (via r-universe)

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Title Fast fitting of MARSS models with TMB

Description Companion to the MARSS package. Fast fitting of MARSS models with TMB. See the MARSS documentation. All the model syntax and features are the same as for the MARSS package.

Version 0.0.14

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URL <https://atsa-es.github.io/marssTMB>,
<https://github.com/atsa-es/marssTMB>

BugReports <https://github.com/atsa-es/marssTMB/issues>

License GPL (>= 2)

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dfaTMB	<i>Tim Cline's original code to Fit a DFA model with TMB.</i>
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Description

This can be called to fit a DFA with his syntax, but generally no work should be done here.

Usage

```
dfaTMB(  
  y,  
  model = list(m = 1, R = "diagonal and equal"),  
  inits = list(R = 0.05),  
  EstCovar = FALSE,  
  Covars = NULL,  
  indivCovar = FALSE,  
  Dmat = NULL,  
  Dfac = NULL,  
  EstSE = FALSE,  
  silent = TRUE,  
  fun.opt = c("nlminb", "optim", "nlminb+optim"),  
  method = c("Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN", "Brent"),  
  control = NULL,  
  form = c("dfa", "marxss")  
)
```

Arguments

y	Vector of observations n x T.
model	list with • R "diagonal and equal", "unconstrained", "diagonal and unequal" • m number of states (x)
inits	list of initial conditions
EstCovar	TRUE/FALSE
Covars	An optional matrix, dimensioned nD x T, where nD is the number of covariates

<code>indivCovar</code>	flag for structure of covariates
<code>Dmat</code>	D initial matrix
<code>Dfac</code>	What elements of D are fixed
<code>EstSE</code>	TRUE / FALSE, whether to return the Hessian from the TMB sdreport
<code>silent</code>	Show TMB output when fitting, defaults to TRUE
<code>fun.opt</code>	function to use for optimization: <code>stats::nlminb()</code> or <code>stats::optim()</code>
<code>method</code>	to pass to optim call; ignored for <code>fun="nlminb"</code>
<code>control</code>	a list with the control settings for the optimization function. See details for the defaults.
<code>form</code>	The equation form used in the <code>marssTMB()</code> call. The default is "dfa".

Details

The control defaults for `stats::nlminb()` are `iter.max = 2000` and `eval.max = 2000`. For `stats::optim()`, the defaults are `reltol = 1e-12` and `maxit = 2000`.

Value

A list with Optimization, Estimates, Fits, and AIC

Author(s)

Tim Cline wrote most of this while a graduate student in the Fish 507 Time Series Analysis course. Eli Holmes later modified it to replicate the MARSS(x, form="dfa") model.

Examples

```
library(MARSS)
data(lakeWAp plankton, package = "MARSS")
phytoplankton <- c("Cryptomonas", "Diatoms", "Greens", "Unicells", "Other.algae")
dat <- as.data.frame(lakeWAp planktonTrans) |>
  subset(Year >= 1980 & Year <= 1989) |>
  subset(select=phytoplankton) |>
  t() |>
  MARSS::zscore()

#fit with MARSS
m1.em <- MARSS(dat, model=list(R='unconstrained', m=1, tinitx=1), form='dfa', z.score=FALSE)
m1.tmb <- dfaTMB(dat, model=list(R='unconstrained', m=1))
c(m1.em$logLik, m1.tmb$logLik)
```

estimate_marss

Internal function: MARSS parameter estimation using TMB

Description

This model is in the general "marss" vectorized form. The diagonals and offdiagonals of R and Q are split apart like Tim Cline did. In `estimate_marss2()`, I use instead the approach in `MARSS::MARSSoptim()` where I just use the `chol()` of these matrices. Technically there are 2 equal solutions since the diagonals appear as the square so -a and a are the same. But I have not observed that this affects the behavior of `optim()`.

Usage

```
estimate_marss(
  MLEobj,
  method = c("TMB", "nlminb_TMB", "BFGS_TMB"),
  opt.control = NULL,
  ...
)
```

Arguments

MLEobj	A properly formatted MARSS model as output by <code>MARSS()</code>
method	Normally passed in as <code>MLEobj\$method</code> , but allows user to pass in a new method if they want to use <code>MLEobj</code> with another method. Allowed values are "TMB", "nlminb.TMB", "BFGS.TMB".
opt.control	Normally this is passed in as <code>MLEobj\$control</code> , but if the <code>MLEobj</code> was set up using a different method, then you will need to set the <code>opt.control</code> options. See details.
...	not used

Details

Minimal error checking is done in this function. Normal calling function is `MARSS::MARSS()` with `method="TMB"`.

The main thing this does is

- collapse the 3D fixed and free matrices into 2D
- separate out the diag and offdiag parameter elements of R and Q

Restrictions

- V0 fixed (not estimated)
- Q and R cannot be time-varying (at the moment)

`opt.control` is what is passed to the control argument in `nlminb()` or `optim()`. If you use `MARSS(x, method="TMB")`, this will be set to appropriate defaults which you can see via `MLEobj$control`. But if you call `estimate_marss()` with a `MLEobj` from a call such as `MARSS(x, method="kem")` (so not a TMB method), you will need to set `opt.control` if you want values different from the base defaults for those functions. Note as a shortcut for `nlminb()`, you can set both `eval.max`, `iter.max` to the same value with `opt.control=list(maxit=1000)`. Note, if you pass in `opt.control`, this will replace all values currently in `MLEobj$control` that are associated with the optimizer function.

The defaults set in `MARSS::MARSS()` are

- `nlminb`: `eval.max = 5000`, `iter.max = 5000` and `trace = 0`.
- `optim`: `maxit = 5000` and `trace = 0`

All other controls for the optimization function are left at `NULL`.

Value

A list with the objective and optimization objects.

- `obj` is the raw output from the `TMB::MakeADFun()` call.
- `op` is the raw output from the optimization call (`optim` or `nlminb`). Note that the function is minimizing the negative log-likelihood so the sign will be opposite of the log-likelihood reported by `MARSS()`
- `opt.control` is the controls sent to the optimization function.
- `method` method used for optimization

Author(s)

Eli Holmes.

See Also

`MARSS::MARSSoptim()`, `MARSS::MARSSkem()`

Examples

```
library(MARSS)
data(lakeWAplankton, package = "MARSS")
phytoplankton <- c("Cryptomonas", "Diatoms", "Greens", "Unicells", "Other.algae")
dat <- as.data.frame(lakeWAplanktonTrans) |>
  subset(Year >= 1980 & Year <= 1989) |>
  subset(select=phytoplankton) |>
  t() |>
  MARSS::zscore()

# set-up the model
mod <- MARSS(dat, model=list(m=3, tinitx=1), form="dfa", fit=FALSE, silent=TRUE)
# fit
fit <- estimate_marss(mod)
```

estimate_marss2

Internal function: MARSS parameter estimation using TMB

Description

This model is in the general "marss" vectorized form. In `estimate_marss2()`, I use the approach in `MARSS::MARSSoptim()` where I just use the `chol()` of these matrices. Technically there are 2 equal solutions since the diagonals appear as the square so -a and a are the same. But I have not observed that this affects the LL of `optim()` but it definitely seems to slow things down. In `estimate_marss()`, the diagonals and offdiagonals of R and Q are split apart like Tim Cline did. I had some problems with the splitting approach for some models with Q unconstrained, though now it seems fixed.

Usage

```
estimate_marss2(
  MLEobj,
  method = c("TMB", "nllminb_TMB", "BFGS_TMB"),
  opt.control = NULL,
  ...
)
```

Arguments

MLEobj	A properly formatted MARSS model as output by <code>MARSS()</code>
method	Normally passed in as <code>MLEobj\$method</code> , but allows user to pass in a new method if they want to use <code>MLEobj</code> with another method. Allowed values are "TMB", "nllminb.TMB", "BFGS.TMB".
opt.control	Normally this is passed in as <code>MLEobj\$control</code> , but if the <code>MLEobj</code> was set up using a different method, then you will need to set the <code>opt.control</code> options. See details.
...	not used

Details

Minimal error checking is done in this function. Normal calling function is `MARSS::MARSS()` with `method="TMB"`.

The main thing this does is

- collapse the 3D fixed and free matrices into 2D
- separate out the diag and offdiag parameter elements of R and Q

Restrictions

- V0 fixed (not estimated)
- Q and R cannot be time-varying (at the moment)

`opt.control` is what is passed to the control argument in `nlminb()` or `optim()`. If you use `MARSS(x, method="TMB")`, this will be set to appropriate defaults which you can see via `MLEobj$control`. But if you call `estimate_marss()` with a `MLEobj` from a call such as `MARSS(x, method="kem")` (so not a TMB method), you will need to set `opt.control` if you want values different from the base defaults for those functions. Note as a shortcut for `nlminb()`, you can set both `eval.max`, `iter.max` to the same value with `opt.control=list(maxit=1000)`. Note, if you pass in `opt.control`, this will replace all values currently in `MLEobj$control` that are associated with the optimizer function.

The defaults set in `MARSS::MARSS()` are

- `nlminb`: `eval.max = 5000`, `iter.max = 5000` and `trace = 0`.
- `optim`: `maxit = 5000` and `trace = 0`

All other controls for the optimization function are left at `NULL`.

Value

A list with the objective and optimization objects.

- `obj` is the raw output from the `TMB::MakeADFun()` call.
- `op` is the raw output from the optimization call (`optim` or `nlminb`). Note that the function is minimizing the negative log-likelihood so the sign will be opposite of the log-likelihood reported by `MARSS()`
- `opt.control` is the controls sent to the optimization function.
- `method` method used for optimization

Author(s)

Eli Holmes.

See Also

`MARSS::MARSSoptim()`, `MARSS::MARSSkem()`

Examples

```
library(MARSS)
data(lakeWAplankton, package = "MARSS")
phytoplankton <- c("Cryptomonas", "Diatoms", "Greens", "Unicells", "Other.algae")
dat <- as.data.frame(lakeWAplanktonTrans) |>
  subset(Year >= 1980 & Year <= 1989) |>
  subset(select=phytoplankton) |>
  t() |>
  MARSS::zscore()

# set-up the model
mod <- MARSS(dat, model=list(m=3, tinitx=1), form="dfa", fit=FALSE, silent=TRUE)
# fit
fit <- estimate_marss(mod)
```

Description

This takes a [MARSS::marssMLE](#) object (fitted or not) and estimates parameters. Note this is the TMB method for the [MARSS::MARSSfit](#) generic. The typical use would be to call as `MARSS(data, method="TMB")`.

Usage

```
## S3 method for class 'TMB'
MARSSfit(x, fun = 1, ...)
```

Arguments

<code>x</code>	A properly formatted MARSS::marssMLE object ready for fitting.
<code>fun</code>	A debugging option to switch between <code>estimate_marss()</code> and <code>estimate_marss2()</code>
<code>...</code>	not used

Details

Restrictions

- V0 fixed (not estimated)
- Q and R cannot be time-varying (at the moment)

`opt.control` is what is passed to the control argument in `nlminb()` or `optim()`. If you use `fit <- MARSS(data, method="TMB")`, this will be set to appropriate defaults which you can see via `fit$control`. But if you call `estimate_marss()` with a `marssMLE` object from a call such as `MARSS(data, method="kem")` (so not a TMB method), you will need to set `opt.control` if you want values different from the base defaults for those functions. Note as a shortcut for `nlminb()`, you can set both `eval.max`, `iter.max` to the same value with `opt.control=list(maxit=1000)`. Note, if you pass in `opt.control`, this will replace all values currently in `fit$control` that are associated with the optimizer function.

The defaults set in [MARSS::MARSS\(\)](#) are

- `nlminb`: `eval.max = 5000`, `iter.max = 5000` and `trace = 0`.
- `optim`: `maxit = 5000` and `trace = 0`

All other controls for the optimization function are left at NULL. You can set other controls in the call `MARSS(..., control=list(...))`.

Value

The `MARSS::marssMLE` object which was passed in, with additional components:

- `method`: From the call or argument `method` if user passed that in.
- `kf`: Kalman filter output.
- `iter.record`: If `x$control$trace = TRUE`, then this is the `$message` value from `stats::optim()` or `stats::nlminb()` plus the output from the `TMB::MakeADFun()` call and the output from the optimization function.
- `numIter`: Number of iterations needed for convergence.
- `convergence`: Did estimation converge successfully?
 - `convergence=0`: Converged in less than `x$control$maxit` iterations and no evidence of degenerate solution.
 - `convergence=3`: No convergence diagnostics were computed because all parameters were fixed thus no fitting required.
 - `convergence=-1`: No convergence diagnostics were computed because the MLE object was not fit (called with `fit=FALSE`). This is not a convergence error just information. There is not `par` element so no functions can be run with the object.
 - `convergence=1`: Maximum number of iterations `x$control$maxit` was reached before convergence.
 - For other convergence errors, see `stats::optim()` or `stats::nlminb()`.
- `logLik`: Log-likelihood.
- `states`: State estimates from the Kalman smoother.
- `states.se`: Confidence intervals based on state standard errors, see caption of Fig 6.3 (p. 337) in Shumway & Stoffer (2006).
- `errors`: Any error messages.

Author(s)

Eli Holmes.

See Also

`MARSS::MARSSoptim()`, `MARSS::MARSSkem()`

`marssTMB_CheckPackageVersions`

Check TMB and Matrix versions

Description

Helper function to provide instructions if there is a mis-match

Usage

```
marssTMB_CheckPackageVersions(silent = TRUE)
```

Arguments

silent Default is TRUE. If FALSE, then gives the full instructions

var_to_cholvar *Return R, Q and V0 with free and par for chol of matrix*

Description

The free, fixed and par (and start) return the vec of the var-cov matrix M: $\text{fixed} + \text{free} \%*\% \text{p} = \text{vec}(M)$. This function transforms the free, fixed, par and start so that they return the chol of the varcov matrix: $\text{vec}(\text{chol}(M))$.

Usage

```
var_to_cholvar(MLEobj)
```

Arguments

MLEobj A properly formatted MARSS model as output by [MARSS\(\)](#)

Details

Why does this function solve for the new par rather than just putting the chol values in? Because the user might have scrambled the order of the parameter list. I won't know which par correspond to which elements of the var-cov matrix. The free matrix is what does the sorting/permutation of the estimated parameters into their correct places. Also the matrix might be block-diagonal, partially fixed, etc.

Restrictions

- Q and R cannot be time-varying (at the moment)

Value

A new [MARSS::marssMLE](#) object with new fixed, free, par and start

Author(s)

Eli Holmes.

Examples

```
dat <- t(harborSealWA)[2:4, ]
fit <- MARSS(dat, model=list(Q="unconstrained"))
fitchol <- var_to_cholvar(fit)
Qchol = coef(fitchol, type="matrix")$Q
Q = coef(fit, type="matrix")$Q
Q
crossprod(Qchol)
```

```
Q = coef(fit, type="matrix", what="start")$Q
Qchol = coef(fitchol, type="matrix", what="start")$Q
Q
crossprod(Qchol)

fit <- MARSS(dat, model=list(Q=diag(0.1,3)+0.01), control=list(maxit=15))
fitchol <- var_to_cholvar(fit)
Qchol = coef(fitchol, type="matrix")$Q
Q = coef(fit, type="matrix")$Q
Q
crossprod(Qchol)
Q = coef(fit, type="matrix", what="start")$Q
Qchol = coef(fitchol, type="matrix", what="start")$Q
Q
crossprod(Qchol)
```

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